

## AMENDMENT

### AMENDMENTS TO THE SPECIFICATION:

Please delete the Sequence Listing and insert therefor the substitute Sequence Listing submitted as text concurrently herewith through EFS-Web.

At page 20, lines 17 through 25, please replace the paragraph with the following paragraph:

Another preferred pH-dependent membrane-binding internalizing peptide in this regard is aa1-aa2-aa3-EAALA(EALA)4-EAL EALAA-amide (SEQ ID NO:601), which represents a modification of the peptide sequence of Subbarao et al. (1987). Within this peptide sequence, the first amino acid residue (aa1) is preferably a unique residue, such as C or K, that facilitates chemical conjugation of the internalizing peptide to a targeting protein conjugate. Amino acid residues 2-3 may be selected to modulate the affinity of the internalizing peptide for different membranes. For instance, if both residues 2 and 3 are K or R, the internalizing peptide will have the capacity to bind to membranes or patches of lipids having a negative surface charge. If residues 2-3 are neutral amino acids, the internalizing peptide will insert into neutral membranes.

At page 35 through page 48, please replace Table 3 with the following Table 3:

**Table 3**  
PIDZ Domains Used in Screening Assays

Gene Name	GI or Acc#	PIDZ#	Sequence fused to GST Construct	SEQ ID NO:
26s subunit p27	9184389	1	RDMAEAHKEAMSRKLGQSESQGPPRAFAK VNSISP GSPSI AGLQVDDEIVEFGSVNTQNFQSLHNI GSVVQHSE GALAPT ILLSVSM	191
AF6	430993	1	LRKEPEITVTLKKQNGMGLSIVA AAKGAGQDKLGIYVKSV VKGGAADV DGRLAAGDQLLSVDGRSLVGLSQERAAELM TRTSSVVTLEVAKQG	192
AIPC	12751451	1	LIRPSVISIIGLYKEKGKGLGFSIAGGRDCIRGQMGI FVKTI FPNGSAAEDGRLKEGDEILDVNGIPIKGLTFQEAHITFKQI RSGLFVLTVRTKLVSPLTNSS	193
AIPC	12751451	2	GISSLGRKTPGPKDRIVMEVTLNKEPRVGLGIGACCLALE NSPPGIYIHS LAPGSVAKMESNL SRGDQILEVNSVNV RHA ALSKVHAILSKC PPGPVRLVIGRHNPVKVSEQEMDEV IAR	194

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO.
			STYQESKEANSS	
AIPC	12751451	3	QSENEEDVCFIVLNRKEGSGLGFSVAGGTDVEPKSITVHR VFSQGAASQEGTMNRGDFLLSVNGASLAGLAHGNVLKV LHQALQHLKDALVVIKKGMDQPRPSNSS	195
AIPC	12751451	4	LGRSVAVHDALCVEVLKTSAGLGLSLDGGKSSVTGDGPI VIKRVYKGGAAEQAGIEAGDEILAINGKPLVGLMHFDA WNIMKSVPEGPVQLLIRKHNSS	196
alpha actinin-2 associated LIM protein APXL-1	2773059	1	REEGMPQTIVLPGPAAWGFRLSGGIDFNQPLVITRITPGS KAAAANLCPGDVILADGFGTESMTHADGQDRIKAAAIIQ LCLKIDRGETHLWSPHSIV	197
	13651263	1	ILVEVQLSGGAPWGFTLKGGRHGEPLVITKIEEGSKAAA VDKLLAGDEIVGINDIGLSGRFQEAICLVKGSHTLKLTV KRNS	198
Atrophin-1 Interacting Protein	2947231	1	REKPLFTRDASQLKGTFLSITLKKSNMGFGFTIIGGDEPDE FLQVKSVIPDGPAAQDGKMETGDVIVINEVCVLGHTHA DVVKLFQSVPIGQSVNLVLCRGYP	199
Atrophin-1 Interacting Protein	2947231	2	LSGATQAEMLMTLTVKGAQGFGFTIADSPGQRVKQILDI QGPCPLGCEGLDIVEINQNVQNLSHTEVVDILKDCPIGSET SLIHRGGFF	200
Atrophin-1 Interacting Protein	2947231	3	HYKELDVHLRRMESGFGFRILGGDEPGQPILIGAVIAMS ADDRGLRHPGDELVYVDGIPVAGKTHRYVIDLMHHAAR NGQVNLTVRRKVLGCG	201
Atrophin-1 Interacting Protein	2947231	4	EGRGISSISLQTSDAVIHRKENEGFGFVISSILNRPI:SGSTIT VPHKIGRIIDGSPADRCACLKVGDRILAVNGQSIIINMPHA DIVKLIKDAGLSVTLRIIPQEEL	202
Atrophin-1 Interacting Protein	2947231	5	LSDYRQPQDFDYFTVDMKGAKGFGFSIRGGREYKMDL YYLRLAEDGPAIRNGMRVGDQIIEINGESTRDMTHARAI ELIKSGGRRVRLLLKRGTTQ	203
Atrophin-1 Interacting Protein	2947231	6	HESVIGRNPEGQLGFELKGAENGQFPYLGEVKPGKVAY ESGSKLVSEELLLEVNETPVAGLTIRDVLAVIKHCKDPLR LKCCKQGGIHR	204
CARD11	12382772	1	SVGHVVRGPGPSVQHTTLNGDSLTSQLTLLGNGARGSVFH SVKPGSLAEKAGLREGHQLLLLLEGICIRGERQSVPLDCTCK EEAHWTIQRCSGPVTLHYKVNHEGYRK	205
CARD14	13129123	1	RRPARRILSQVTMLAFQGDALLEQISVIGGNLTGFIHVRV PGSAADQMALRPQTQIVMVDYEASEPLFAVLEDTTLEE AVGLLRVRVDGFCCLSVKVNVDGYKR (SEQ ID NO:445)	206
CASK	3087815	1	TRVRLVQFQKNTDEPMGITLKMNELNHCIVARIMHGGMI IHQGTLLHVGEIREINGISVANQTVELQKMLREMRGSI FKIVPSYRTQS	207
Connector Enhancer	3930780	1	LEQKAVLEQVQLDSPLGLEIHTTSNCQHFSVQVDTVQPTD SRLQIQPGEDEVVQINEQVVVGWPRKNMVRELLREPAGLS LVLLKKIPI	208
Cytoshesin Binding Protein	3192908	1	QRKLVTVEKQDNETFGFIEQSYRPQNQNACSSEMFTLICK IQEDSPAHCAGLQAGDVLANINGVSTEGFTYKQVVDLIRS SGNLLTIETLNG	209

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
Densin 180	16755892	1	RCLIQTKGQRSMGYPEQFCVRIEKNPGLGFSISGGISCGG NPFKPSDKGIFVTRVQPDGPASNLLQPGDKILQANGHSFV HMEHEKAVLLLSKFQNTVDLVIQRELTV	210
DLG1	475816	1	IQVNGTDADYEYEEITLERGNSGLGFSIAGGTDNPHIGDD SSIFITKIITGGAAQDGRLLRVNDCILQVNEVDVRDVTHSK AVEALKEAGSIVRLYVKRRN	211
DLG1	475816	2	IQLIKGPKGLGFSIAGGVGNQHIPGDNISYVTKIIEGGAH KDGKLGIGDKLLAVNNVCLEEVTHEEAVALTKNTSDFVY LKVAKPTSMYMNDGN	212
DLG1	475816	3	ILHRGSTGLGFNIVGGEDGEGIFISFILAGGPADLSGELRKG DRIISVNSVDLRAASHEQAAAAALKNAGQAVTIVAQYRPE EYSR	213
DLG2	12736552	1	ISYVNGTEIEYEFEEITLERGNSGLGFSIAGGTDNPHIGDDP GIFITKIIPGGAAAEDGRI.RVNDCILRVNEVDVSEVSHSKA VEALKEAGSIVRLYVRRR	214
DLG2	12736552	2	IPILETVVEIKLFKGPGLGFSIAGGVGNQHIPGDNISYVTK IIDGGAAQKDGRLQVGDRLLMVNNYSLEEVTHEEAVAL KNTSEVVYLVKVGKPTTIVMTDPYGPNNSS	215
DLG2	12736552	3	ILEGEPKRVVLHKGSTGLGFNIVGGEDGEGIFVSFILAGGP ADLSGELQRGDQILSVNGIDLRGASHEQAAAAALKAGQT VTIIAQHQPEDYARFEAKIHDLSN	216
DLG5	3650451	1	GIPYVEEPRHVKVQKGSEPLGISIVSGEKGGIYVSKVTGVS IAHQAGLEYGDQLLEFNGLNRSATEQQARLIIGQQCDTIT ILAQYNPHVHQLRNSZLTD	217
DLG5	3650451	2	GILAGDANKTKLEPRVVFIIKKSQLELGVHLCCGNLHGVF VAEVEDDSPAKGPDGLVPGDLILEYGSGLDVRNKTVEEVY VEMLKPRDGVRLKVQYRPEEFIVTD	218
DLG6, splice variant 1	14647140	1	PTSPEIQELRQMLQAPHFKALLSAHDTIAQKDFEPLLPPLP DNIPSEEEAMRIVCLVKNQQPLGATIKRHEMTGDILVARI HGGIAERSGLLYAGDKLVEVNGVSVEGLDPEQVIHILAMSRG SRGTIMFKVVPVSDPPVNSS	219
DLG6, splice variant 2	AB053303	1	PTSPEIQELRQMLQAPHFKGATIKRHEMTGDILVARIHGG LAERSGLLYAGDKLVEVNGVSVEGLDPEQVIHILAMSRG TIMFKVVPVSDPPVNSS	220
DVL1	2291005	1	LNIVTVTLNMRHHFLGISIVGQSNDRGDGGIYIGSIMKG GAVAADGRIEPPGDMLLQVNDVNFENMSNDDAVRVLREI VSQTGPISLTVAKCW	221
DVL2	2291007	1	LNITVTNLNMEKYNFLGISIVGQSNDRGDGGIYIGSIMKGG AVAADGRIEPPGDMLLQVNDVNFENMSNDDAVRVLRDIV IIPGPPIVLTVAKCWDPSQNS	222
DVL3	6806886	1	IITVTNLNMEKYNFLGISIVGQSNDRGDGGIYIGSIMKGGAV AADGRIEPPGDMLLQVNEINFENMSNDDAVRVLREIIVIKP GPITLTVAKCWDPSP	223
ELFIN 1	2957144	1	LTTQQIDLQGPWPWGFRLVGRKDFEQPLAISRVTPGSKAA LANLCIGDVITAIIDGENTSNMTHLEAQNRKIGCTDNLTLT VARSEHKVWSPVLTNSS	224
ENIGMA	561636	1	IFMDSFKVVLEGPAPWGFRLQGGKDFNVPLSISRLTPGGK AAQAGVAVGDWVLSIDGENAGSLTHIEAQNKIRACGERL	225

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
			SLGLSRAQPV	
ERBIN	8923908	1	QGHELAKQEI RVRVEKDPELGFSSISGGVGGGRGNPFRPDDDD GIFVTRVQPEGPASKLLQPGDKIIQANGYSFINIEIHQGA V S L L K T F Q N T V E L I I V R E V S S	226
EZRIN Binding Protein 50	3220018	1	QMSADA AAGAPL PRLCCLEKGPNGYGFHLHGEKGLGQ YIRLVEPGSPA EKAGLLAGDRLVEVNGENVEKETHHQVV SRIRAAALNAVRLLVDPETDEQLQKLGVQVREELLRAQE APGQAEPPAAAEEVQGAGNENEPREADKSHPEQRELNNSS	227
EZRIN Binding Protein 50	3220018	2	IQQRELRLPRLCTMKKGPSGYGFNLHSDKSKPGQFIRSVDP DSPAEASGLRAQDRIVEVNGVCMEGKQHGDVVS AIRAG GDETCLLVVDRETDEFFKNSS	228
FLJ00011	10440352	1	KNPSGELKTVTL SKMKQSLGISISGGIESKVQPMVKIEKIF PGGAFLSGALQAGFELVAVDGENLEQVTHQRAVD TIRR AYRNKAREPMELVVRVPGPSRPSPSD	229
FLJ1215	11436365	1	EGHSHPRVVELPKTEEGLGFNIMGGKEQNSPIYISRIIPGGI ADRHGGLKRGDQLLSVNGVSVEGHHHEKAVELLKAAQG KVKLVVRYTPK VLEEME	230
FLJ12428	BC012040	1	PGAPYARKTFTIVGDAVWGWFVVRGSKPCHIQAVDPSGP AAAAGMKVCQFVSVVNGLNLVHVDYRTVSNLITGPRTI VMEVMEELEC	231
FLJ12615	10434209	1	GQYGGETVKIVRIEKARDIPLGATVRNEMDSVHSIRIVKGG AAEKSGLLHEGDEVLEINGIEIRGKDVNEVFDLLSDMHGT LTFVLIPSQIKPPPA	232
FLJ20075	7019938	1	ILAHVKGIEKVN VYKSEDSLGLTITDNGVGYAFIKRIKD GGVIDSVK TICVGDHIESINGENIVGWRHYDVAKKL KELK KEELFTMKLIEPKKAFEI	233
FLJ21687	10437836	1	KPSQASGHFSVELVRGYAGFGLTLGGGRD VAGDTPLAVR GLLKDGP AQRCGRLEVGDVLHNGESTQGLTHAQAV ER IRAGGPQLHLVIRRPLETHPGKPRGV	234
FLJ31349	AK055911	1	PVMSQCACLEEVHLPNIKPGEGLGMYIKSTYDGLHVITGT TENSADR SQKI HAGDEVIQV NQQT VVGWQLKNLVKKL RENPTGVVLLLKKRPTGSFNFTPEFIVTD	235
FLJ32798	AK057360	1	LDDEEDSVKIHRLVKNREPLGATIKKDEQGTGA IIVARIMRG GAADRSLI HVGDELREVN GIPVEDKRPEI IQLAQSQGA ITFKIIPGSKEETPSNSS	236
GoRASP1	NM031899	1	MGLGVSAEQPAGGAEGFHLHGVQENSPAQQAGLEPYFD FITIGHSRNLNKENDTLKALLKANVEKPVKMLIYSSKTLER VREVEV VPSNMWGGQGLLGASVRFC SFRRASE	237
GoRASP1	NM031899	2	RASEQVWHVLDV EPSSPAALAGLRPYTDYVVGSDQILQE SEDFFTLIESHEGKPLKLMVYNSKSDSCREVTVTPNAAW GGEGLGCGIGYGYLHRIPTQ	238
GoRASP2	13994253	1	MGSSQSV EIPGGGTEGYHVLRVQENSPGHRAGLEPFDFPI VSINGSRNLKNDNDTLKDLLKANVEKPVKMLIYSSKTLER ETSVTPSNLWGGQGLLGVSIRFC SFDGANE	239
GoRASP2	13994253	2	NENNVWHVLEVESNSPAALAGLRPHSDYIIGADTVMNESE DLFSLIE THEAKPLKLYVYNTD TDNCREVITTPNSAWGGE GSLGCGIGYGYLHRIPTR	240

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
GRIP 1	4539083	1	VVELMKKEGTTGLTVSGGIDKDGKPRVSNLRQGGIAARDQQLDVGDYIKAVNGINLAKFRHDEHSLLKNVGERVVLEVEYE	241
GRIP 1	4539083	2	RSSVIFRTVEVTLHKEGNTFGFVIRGGAHDDRNSKRPVVI TCVRPGGPADREGTIKPGDRLLSDVGRLLGTTTHAEAMSI LKQCGQEAAALLIEYDVSVMDSVATASGNSS	242
GRIP 1	4539083	3	HVATASGPLLVEVAKTPGASLGVALTTS MCCNKQVIVID KIKSASIADRCGALHVG DHI LSIDGTSMEYCTLA EATQFI. ANT TTDQVKLEILPHHQTRLALKGPNSS	243
GRIP 1	4539083	4	HVATASGPLLVEVAKTPGASLGVALTTS MCCNKQVIVID KIKSASIADRCGALHVG DHI LSIDGTSMEYCTLA EATQFI. ANT TTDQVKLEILPHHQTRLALKGPNSS	244
GRIP 1	4539083	5	AESVIPSSGTFHVKLPKKHNVLEGITISSPSRKP GDPLVIS DIKKGSAVHRTGTLELGDKLLAIDNIRLDNCSMEDAVQIL QQCEDLVKLKIRKDEDNSD	245
GRIP 1	4539083	6	IYTVELKRYGGPLGITISGTEEPFDPHISLTKGGLAERTGA IHIGDRILAINSSSLK GKPLSEAIHLLQ MAGETVTLKIKKQT DAQSA	246
GRIP 1	4539083	7	IMSPTPVLELHKVTLTKYKDSMEDFGFSVADG LLEKGVYVK NIRPAGPGDLGGLKPYDRLLQVNHVTRDRDFCCLLVPLI AESGNKLDLVISRNPLA	247
GTPase Activating Enzyme Guanine Exchange Factor	2389008	1	LSRGCE TRELALPRDGGQRLGFEVDAEGFVTHVERFTFAE TAGLRPGARLLRVCGQTPLPSLRPEAAAQLRSAPKVCVT VLPDESGRPNSS	248
	6650765	1	CSVMIFEVVEQAGAIILEDGQELDSWYVILNGTVEISHPD GKVENLFMGNSFGITPTLDKQYMHGIVRTKVDDCQFVCI AQODYWRILNHVEKNTHKVEEGEIVMVHEFIVTD	249
HEMBA 1000505	10436367	1	LENVIAKSLLIKSNEGSYGFGLDKNKVPIIKLVEKGSNAE MAGMEVGKKIFAINGDLVFMRFNEVDCFLKSCLSNRKP LRVLVSTKP	250
HEMBA 1000505	10436367	2	PRETVKIPDSADGLGFOIRGFGPSVHVAVGRGTVA AAAAG LHPGQCIIKVNGINVSKETHASVIAHVTACRKYRRPTKQD SIQNSS	251
HEMBA 1003117	7022001	1	EDFCYVFTVELERGPSGLGMGLIDGMHTHLGAPGLYIQT L.LPGSPAADGRLSLGDRILEVNGSSLLGLGYLRAVDLIR IIGGKKMRFLVAKSDVETAKKI	252
HSPC227	7106843	1	NNEI.TQFLPRTITLKKPPGAQLGFNIRGGKASQLGIFISKVI PDS DAHRAGLQEGDQVLAVNDVDFQDIEHSKAVEILKTA REISM RVRFPPYNYHROKE	253
HTRA3	AY040094	1	LTEFQDKQIKDWKKRFIGIRMRITITPSLVDELKASNPDPPE VSSGIYVQEVAPNSPSQRGGIQDGIIVKVNGRPLVDSSEL QEAVLTESPLLLEVRNGNDLLFSNSS (SEQ ID NO:158)	254
HTRA4	AL576444	1	HKKYLGQLMSLTVP LSELKMHYPDFDPDVSSGVYVCKV VEGTAAQSSGLRDHDVIVNNGKPIITTTDVVKALDSDSL SMAVLRGKDNL LLLTVNSS	255
INADI.	2370148	1	IWQIEYIDIERPSTGG LGFSVVALRSQNLGKVDIFVKDVQP GSVADRDRQLKENDQILAINHTPLDQNISHQQAIALLOQT TGSLRLIVAREPVHTKSSTSSSE	256

Gene Name	GI or Acc#	PD/#	Sequence fused to GST Construct	SEQ ID NO:
INADL	2370148	2	LPETVCWGHVVEEVLINDGSGLGFIVGGKTSGVVVRTIV PGGLADRDGRLQTGDHILKIGGTNVQGMTSEQVAQVLR NCGNSVRMLVARDPAGDISVTNNS	257
INADL	2370148	3	PGSDSSLFETYNVELVRKDGQSLGIRIVGYVGTSHTEAS GIYVKSIIPGSAAYHNGHIQVNDKIVAVDGVNIQGFANHD VVEVLRNAGQVVHLTLVRRKTSSTSRHHRD	258
INADL	2370148	4	NSDDAELQKYSKLLPIHTLRLGVEVDSFDGHHYISSIVSG GPVDTLGLLQPEDELLEVNGMQLYGKSRREAVSFLKEVP PPFTLVCCRRLLFDDEAS	259
INADL	2370148	5	LSSPEVKIVELVKDCKGLGFSILDYQDPLDPTRSVIVIRSLV ADGVAERSSGGLLPDRLVSVNEYCLDNTSLAEAVEILKA VPPGLVHLGICKPLVEFIVTD	260
INADL	2370148	6	PNFSHWGPPIRVEIFREPNSVLSGISIVVGQTVIKRLKNGEEL KGIFIKQVLEDSAPAGKTNAIKTGDKILEVSGVDLQNASHS EAVEAIKNAGNPVVFVQSLSTPRVIPNVHNKANS	261
INADL	2370148	7	PGELHIIIELEKDKNGLGLSLAGNKDRSRMSIFVVGINPFGP AAADGRMRIGDELLEINNQLIYGRSHQNASAIKTAAPSKV KLVFIRNEDAVNQMANSS	262
INADL	2370148	8	PATCPIVPGQEMIIIEISKGRSGLGLSIVGGKDTPLNAIVIH VYEEGAAARDGRLWAGDQILEVNGVDLRNNSHEEAITAL RQTPQKVRLLVY	263
KIAA0147	1469875	1	ILTLTILRQTGGGLGISIAGGKGSTPYKGDDEGIFISRVSEEG PAARAGVRVGDKLLEVNGVALQGAHEHVEALRGAGT AYQMRVWRERMVEPENAIEFIVTD	264
KIAA0147	1469875	2	PLRQRHVACLARSERGLGFSIAGGKGSTPYRAGDAGIFVS RIAEGGAHRAGTLQVGDRLVLSINGVDVTEARHDHVAVSL LTAASPTIALLEREAGG	265
KIAA0147	1469875	3	ILEGPYPVEEIRLPRAGGPLGLSIVGGSDHSSHPFGVQEPG VFISKVLPRLGAARSGLRVGDRILAVNGQDVRDATHQEA VSALLRPCLELSELLVRRDPAEFIVTD	266
KIAA0147	1469875	4	RELCIQKAPGERLGLSIRGGARGHAGNPRDPTDEGIFISKV SPTGAAGRDGRLRVGLRLLEVNGQSSLLGLTHGEAVQLLR SVGDTLTVLVCDGFEASTDAALEVS	267
KIAA0303	2224546	1	PHQPIVHSSGKNYGFITRAIRVYVGDSDIYTVHHIVWNVE EGSPACQAGLKAGDLITHINGEPVHGLVHTEVIELLLKSG NKVSIITTPF	268
KIAA0313	7657260	1	HLRLNLNIAACAAKAKRRMLMTLTKPSREAPLPFILLGGSEKG FGIFVDSVDSGSKATEAGLKRGDQILEVNGQNFENIQLSK AMEII.RNNTHLSITVKTNLFVFKELLTRLSEEKRNAGPNS	269
KIAA0316	6683123	1	IPAPPRKVEMRDPVLGFGFVAGSEKPVVVRSVTPGGPSE GKLI PGDQIVMINDEPVSAAPRERVIDL.VRSCKESILLTVIQ PYPSPKSEFIVTD	270
KIAA0340	2224620	1	LNKRTTMPKDSGALLGLKVVGKMTDLGRLGAFITKVK KGLADVVGHRLRAGDEVLEWNGKPLPGATNEEVYNIIIIE SKSEPQVEIIVSRPIGDIPRIHRD	271
KIAA0380	2224700	1	QRCVHIIQKDQHGFGFTVSGDRIVLVQSVRPGGAAMKAGV KEGDRIIKVNGTMTVNSSHLEVVKLIKSGAYVALTLTGSS	272

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
K1AA0382	7662087	1	ILVQRCVHQQDDNGFGLTVSGDNPVQSVKEDGAAMRAGVQTGDRHKVNGTLVTHSNHLEVVKLIKSGSYVALTVQGRPPGNSS	273
K1AA0440	2662160	1	SVEMTLRRNGLGQLGFHVNYEGIVADVEPYGYAWQAGLRQGSRLVEICKVAVATLSHEQMIDLLRTSVTVKVVIIPIHD	274
K1AA0545	14762850	1	LKVMTSWETVDMTLRRNGLGQLGFHVKYDGTVAEVEDYGFVWQAGLRQGSRLVEICKVAVVTLTHDQMIIDLLRTSVTVKVVIIPIPFEDGTPRRGW (SEQ ID NO:179)	275
K1AA0559	3043641	1	HYIFPHARIKITRDSKDHTVSGNGLGIRIVGGKEIPGSHGEIGAYIAKILPGGSAEQTGKLMEGMQVLEWNGIPLTSKTYEEVQSIISQQSGEAEICVRLDLNML	276
K1AA0561	3043645	1	LCGSLRPPIVHSSGKKYGFSLRAIRVYMGDSVDVYTVHHVWVSVEDGSPAQEAAGLRAGDLITHINGESSVLGLVHMDVVEILLKSGNKISLRTTALENTSIVGNSS	277
K1AA0613	3327039	1	SYSVTLTGPGPWGFRLLQGGKDFNMPLTISRITPGSKAAQSQLSQGDLVVAIDGVNTDTMTHELAQNKIKSASYNLSLTLQKSKNSS	278
K1AA0751 RIM2	12734165	1	TLNEESHSHDKHPVTWQPSKDGDRLLGRILLNKRIKDGSVPRDSGAMLLGLKVVGKMTESGRICAFITKVKKGSLADTVGHLPDGEVLEWNGRILLQGAATFEVYNIIESKPEPQVELVVSRIPIG	279
K1AA0807	3882334	1	ISALGSMRPPIIIHRAGKKYGFTLRAIRVYMGDSVDVYTVHHMVWHVEDGGPASEAGLRQGDLLITHVNGEPVHGLVHTEVVELILKSGNKVAISTTPLENSS	280
K1AA0858	4240204	1	FSDMRISINQTPGKSLDFGFTIKWDIPGIFVASVEAGSPAEEFSQLQVDDEIIAINTTKFSYNDKSKEWEEAMAKAQETGHLVMDVRRYVGKAGSPE	281
K1AA0902	4240292	1	QSAHLEVIQLANIKPSEGLGMYIKSTYDGLHVITGTITENSPADRCKKIHAGDEVIQVNHQTVVGGWQLKNLVNAILREDPSGVILTLKKRPQSMILTSAPA	282
K1AA0967	4589577	1	ILTQTLIPVRHTVKIDKDTLLQDYGFIHESLPLTVVAVTAGSAHGLKLPFGDQILQMNNEPAEDLSWERAVDILREAEDSLSTVVRCTSGVPKSSNSS	283
K1AA0973	4589589	1	GLRSPITIQRSKKYGFTLRAIRVYMGDTDVYSVHHIVWHVEEGGPAQEAAGLCAGDLITHVNGEPVHGMVHPEVVELILLKSGNKVAVTTTTPE	284
K1AA1095	5889526	1	QGEETKSLTLVLHRDSGSLGFNIIGGRPSVDNHDGSSEGI FVSKIVDSGPAAKEGGLQIHDRIIEVNGRDLSRATHDQAVEAFKTAKEPIVVQVLRRTPRTKMFTPT	285
K1AA1095	5889526	2	QEMDREELEEBVDLYRMNSQDKGLGTLVCYRTDDEDDIGYISEIDPNSIAAKDGRIREGDRIIQINGIEVQNREEFAVALLTSEENKNFSLLIARPELQLD	286
K1AA1202	6330421	1	RSFQYVPVQLQGGAPWGFTLKGGLHEHCEPLTVSKIEDGGKAALSQKMRTGDDELVNINGTPLYGSRQEALILKGSFRILKLIVRRRNAPVS	287
K1AA1222	6330610	1	ILEKILFPVELEKDEDDGLGISHGMGVGADAGLEKLGIFVKVTEGGAAQRDGRIGQVNDQIVEVDGISLVGVTQNFAT	288

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
			VLRNTKGNRVFVIGREKPGQVS	
KIAA1284	6331369	1	KDVNVVYNPKKLTVIKAKEQLKLEVLVGIHQTKWSWR RTGKQGDGERLVVHGLLPGGSAMKSGQVLIGDVLVAVN DVDVTTENIERVLSICPGPMQVKLTFENAYDVKRET	289
KIAA1389	7243158	1	TRGCETVEMTLRRNGLGQLGFHVNFEIGIVADVEPFGFAW KAGLRQGSRLVEICKVAVATLTHEQMIDLLRTSVTVKVVV IQPHDDGSPRR	290
KIAA1415	7243210	1	VENILAKRLLILPQEDYGFDEIEKNKAVVVKSVQRGSLA EVAGLQVGRKIYSINEDLVFLRPFSEVESILNQSFCSRRI RLLVATKAKEIIP (SEQ ID NO:195)	291
KIAA1526	5817166	1	PDSAGPGEVRLVSLRRKAHEGLGFSIRGGSEHGVIYVS LVEPGSLAEKEGLRVGDQILRVNDKSLARVTHAEAVKAL KGSKKLVLSVYSAGRIPGGYVTNHIEFIVTD	292
KIAA1526	5817166	2	LQGGDEKKVNLVLGDGRSLGLTIRGGAEGYGLGIYITGVDP GSEAEAGSLKVGDDQILEVNWRSFLNHLHDEAVRLKSSRH LILTVKDVGRPLPHARTTVDEEFIVTD	293
KIAA1526	5817166	3	WTSGAHVHSGPCEEKCGHPGHRQPLPRIVTIQRGSAHN CGQLKVGHVILEVNLTLRGKEHREAAIIAEAFKTKDR DYIDFLDSL	294
KIAA1620	10047316	1	ELRRAELVEHIVETEAQTGVSGINAVAGGKGEFVRELRED SPAARSLSLQEGDQLLSARVFFENFKYEDALRLQLCAEPY KVSFCLKRTVPTGDLALRP	295
KIAA1634	10047344	1	PSQLKGVLRASLKKSTMFGFTIHGGDRPDEFLQVKNVL KDGPAAQDGKIAPGDVIVDINGNCVLGHTHADVVQMFQ LVPVNYVNLTLRCRGYPLPDDSED	296
KIAA1634	10047344	2	ASSGSSQPELVTIPLIKGPKGFGFAIADSPTGQVKVMILDS QWCQGLQKGDIIEIYHQNVQNLTHLQVVEVLKQFPVGA DVPLLILRGPPSPPTKTAKM	297
KIAA1634	10047344	3	LYEDKPLTNTFLISNPRTTADPRILYEDKPPNTKDLDVFL RKQESGFGFRVLGGDGPDSIYIGAIPLGAAEKDGRLRA ADELMCIDGIPVKGKSHKQVLDLMTTAARNGHVLLTVR RKIFYGEKQPEDDSGSPGIHRELT	298
KIAA1634	10047344	4	PAPQEPYDVVLQRKENEGFGFVILTSKNKPPPGVIPHKIGR VIEGSPADRCGLKVGDHISAVNGQSIVELSHDNIVQLIK DAGVTVTLTVIAEEHHGPPS	299
KIAA1634	10047344	5	QNLGCYPVELERGPRGFGFSLRGGKEYNMGLFILRLAED GPAIKDGRHVGDDQIVEINGEPTQGITHTRAIELIQAGGNK VLLLLRPGTGLIPDHGLA	300
KIAA1719	1267982	0	ITVVLEIKKEGSTLGLTISGGTDKDGKPRVSNLRPGGLAA RSDLLNIGDYIRSVMGIHLTRLRHDEIITLLKNVGERVVIIE VEY	301
KIAA1719	1267982	1	ILDVSLYKEGNSFGFVLRGGAHEDGHKSRLVLTVYVRPG GPADREGSLKVGDRLLSVDGIPLHGASHATALATLRQCS HEALFQVEYDVATP	302
KIAA1719	1267982	2	IHTVANASGLPMVEIVKTPGSALGISLTTTSLRNKSVTIIDR IKPASVVDNRSGALHPGDHILSIDGTSMEHCSSLLEATKLLAS ISEKVRLEILPVPQSQRPL	303



Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
KIAA1719	1267982	3	IQIVHTTETTEVVLCDPLSGFGLQLQGGIFATETLSSPPLV CFIEPDSPAERCGLLQVGDRLVLSINGIA TEDGTMEEANQL LRDAALAHKVVLEVEFDVAESV	304
KIAA1719	1267982	4	IQFDVAESVIPSSGTFHVKLPKKRSVELGITISSASRRKGE LIISDIKKGSVAHRTGTLEPGDKLLAIDNRLDNCMPEDAV QLRQCEDLVKLKIRKDEDN	305
KIAA1719	1267982	5	IQTTGAVSYTVELKRYGGPLGITISGTEEPFDPVIVSLTKR GLAERTGAHVGDRLAINNVS LKGRPLSEAIHLLQVAGE TVTLKIKKQLDR )	306
KIAA1719	1267982	6	I LEMEELLPTPLEMHKVTLHKDPMRHDFGSVSDGLEEK GVYVHTVRPDGPAHRGGLQPFDRVLQVNVHVRTRDFDCC LAVPLLAEGDVLELIISRKPHTAHSS	307
LIM Mystique	12734250	1	MALTVDVAGPAPWGFRTTGGRRDFTHTPIMVTKVAERGKA KDADLRPGDIIVAINGESAEAGMLHAEAQSKIRQSPSPRLRQ LDRSQATSPGQT	308
LIM Protein	3108092	1	SNYSVSLVGPAPWGFRLQGGKDFNMPLTISSLDKGKAA QANVRIGDVLSDIGINAQGMTHLEAQNKIKGCTGSLNM TLQRAS	309
LIMK1	4587498	1	TLVEHSKLYCGHCYYQT VVTPVIEQILPDSPGSHLPHTVT LVSIPASSHGKRLSVSIDPPHGGPGCGTEHSHTVRVQGV DPGCMSPDVKNSHVGDRIIEINGTPIRNVPLDEIDLIIQET SRLLQLTLEHD	310
LIMK2	1805593	1	PYSVTLISMPATTEGRRGFSVSVESACSNYATTVQVKEVN RMHISPNNRNIAHPGDRILEINGTPVRTLRVEVEDAISQT SQTLQLLIEHD	311
LIM-RIL	1085021	1	IHSVTLRGSPWGFRLVGRDFSAPLTISR VHAGSKASLAA LCPGDLIAINGESTELMTHLEAQNRIKGCHDHLTISVSR PE	312
LU-1	U52111	1	VCYRTDDEEDLGIVYGEVNPNSIAAKDGRIREGDRIIQING VDVQNREEAVAILSQEENTNISLLVARPESQLA	313
MAG11	3370997	1	PSELKKGKFIHTKLKSSRGFGFTVVGDEPDEFIQIKSLVL DGPAALDGKMETGDVIVSVNDTCVLGHTHAQVVKIFQSI PIGASVDLELCRGYPLFPDGDGIHRD	314
MAG11	3370997	2	PATQPELITVHIVKGPMSGFTIADSPGGGGQRVKQIVDSP RCRGLKEGDLIVEVNNKKNVQALTHNQVVDMLVECPKGS EVTLLVQRGGNSSZ	315
MAG11	3370997	3	QATQEQDFYTVELERGAKGFGFSLRGGREYNMDLYVLR LAEDGPAERCCKMRIGDEILEINGETTKNMKHSRAIELIK NGGRRVRLFLKRG	316
MAG11	3370997	4	PGVVSTVVQPYDVEIRRGGENEGFGFVIVSVSRPEAGTTF AGNACVAMPHKIGRIIEGSPADRCGLKVGDRILAVNGC SITNKSHDIVNLIKEAGNTVTLRIIPGDESSNAEFIVTD	317
MAG11	3370997	5	PDYQEQDIFLWRKETGFGFRILGGNEPGEPIYIGHIVPLGA ADTDGRLRSGDELICVDGTPVIGKSHQLVVQLMQQAAKQ GHNLTIVRRKVVFAVPKTENSS	318
MGC5395	BC01247 7	1	PAKMEKEETTRELLPNWQGSGLHTIAQRDDGVFVQIE VTQNSPAARTGVVKEGDQIVGATIFYDNLSQGEVTQLLN TMGHHTVGLKLHRKGDRSPNSS	319

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
MINT1	2625024	1	SENCKdVFIEKQKGEILGVVIVESGWSILPTVIANMMHGGPAEKSGKLNIGDQIMSINGTSLVGLPLSTCQSIHKGLKNQSRVKLNIVRCPPVNSS	320
MINT1	2625024	2	LRCPPVTTVLIRRPDLRYQLGFSVQNGIHCSLMRGGIAERG GVRVGHRIIEINGQSVVATPHEKIVHILSNAVGEIHMKTMPAAMYRLNNS	321
MINT3	3169808	1	HNGDLDHFSNSDNCREVHLEKRRGEGGLVALVESGWSGLLPTAVIANLLHGGPAERSGALSIGDRLTAINGTSLVGLPLAACQAAVRETKSQTSVTLIVHCPPVT	322
MINT3	3169808	2	PVTTAIIHRPHAREQLGFCVEDGHICSLRGGIAERGGIRVGHRIIEINGQSVVATPHARIEELLTEAYGEVHIKTMPAATYRLLTG NSS	323
MPP1	189785	1	RKVRILQFEKVTEPMGITLKLNEKQSCVAVRILHGGMIHROGSLHVGDIEILINGTNVTNHSVDQLQKAMKETKGMISLKVIPNQ	324
MPP2	939884	1	PVPPDAVRMVGIRKTAGEHLGVTFRVEGGELVIARILHGGMVAQQGLLHVGDIIKEVNGQPVGSDPRALQELLRNASGSVILKILPNYQ	325
MPP3	1022812	1	NIDEDFDES VKIVRLVKNKEPLGATIRRDHESGAVVVARIMRGGAADRSGLVHVGDDELREVNGIAVLHKKRPDEISQILAQSGSITLKIIPATQEEDR	326
MUPP1	2104784	1	QGRHVEVFELKPPSGGLGFSVVGRLSENREGELGIFVQEIQEGSVAHRDGRLLKETDQILAINGQALDQTITTHQQAISILQKAKDTQLVVIARGSLPQLV	327
MUPP1	2104784	2	PVHWQHMETIELVNDGSGLGFGIIGGKATGVIVKLTILPGGVADQHGRLLCSGDHILKIGDITDLAGMSSEQVAQVLRQCGNRVKLMIARGAIEERTAPT	328
MUPP1	2104784	3	QESETFDELTKNVQGLGITIAGYIGDKKLEPSGIFVKISITKSSAVEHDGRIQIGDQIIAVDGTNLQGFNTQQA VEVLRIHTGQTVLLTLMRRGMKQEA	329
MUPP1	2104784	4	LYEIVVAHVSKFSSENSGLGISLEATVGHHFIRSVLPEGPVGHSGKLFSGDELLEVNGITLLGENHQDVVNILKEIPIEVTMVCRRRTVPPT	330
MUPP1	2104784	5	WEAGIQHIELEKSGKGLGFSILDYQDPIDPASTVHIIRSLVPGGIAEKDGRLLPGDRMLFVNDVNLNSSLEEA VEALKGA PSGTVRIGVAKPLPLSPEENSS	331
MUPP1	2104784	6	RNVSKESFERTINIAKGNSSLGMTVSANKDGLGMIVRSIIHGGAISRDGRIAGDCILSINEESTISVTNAQARAMLRHSLIGPDIKITYVPAEHLEE	332
MUPP1	2104784	7	LNWNQPRRVELWREPSKSLGISIVGGRGMGSRLSNGEVMRGIFIKHVLEDSPAGKNGTLKPGDRIVEVDGMDLRDASHIEQAVEAIRKAGNPVVFVMQSIINRPKSLPSLL	333
MUPP1	2104784	8	LTGELHMIIELEKHSGLGLSLAGNKDRSRMSVFIVGIDPNGAAGKDGRLLQIADELLEINGQILYGRSHQNASSIHKCAPSKVKIIFIRNKDAVNQ	334
MUPP1	2104784	9	LSSFKNVQHLELPKDQGGGLGIAISEEDTLSGVVIKSLTEHGVAAATDGRLLKVGDDILAVDDEIVVGYPIEFISLLKTKAKMTVKLTIHAENPDSQ	335

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO.
MUPPI	2104784	10	LPGCETTIEISKGRITGLGLSIVGGSDTLGAIHIEVYEEGA ACKDGRLLWAGDQILEVNGIDLKATHDEAINVLRQTPQR VRLTLRYDEAPYKE	336
MUPPI	2104784	11	KEEEVCDTLTIELQKKPGKGLGLSIVGKRNDTGTVFVSDIV KGGIADADGRLLMQGQDQLMVNGEDVRNATQEAVALLLK CSLGTVTLEVGRIKAGPFHS	337
MUPPI	2104784	12	LQGLRTVEMKKGPITDSLGISAGGVGSGPLGDVPFIAMMIH PTGVAQAQTKLRVGDRIVTICGTSTEGMTHTQAVNLLKN ASGSIEMQVVAGGDVSV	338
MUPPI	2104784	13	LGPPOCKSITLERGPDGLGFSIVGGYSGPHGLPIYVKTVE AKGAASEDGRLLKRGDQIIHAVNGQSLEGVTHEEAVAILKR TKGTVTLMVLS	339
NeDLG	10863920	1	IQYEEIVLERGNSGLGFSIAGGIDNPHVPDDPGFITKIIPGG AAAMDGRLLGVNDCLVRVNEVEVSEVHSRAVEALKEA GPVVRLLVRRRQN	340
NeDLG	10863920	2	ITLLKGPKGLGFSIAGGIGNQHIPGDNSIYITKIIIEGGAQK DGRLLQIGDRLLAVNNNTNLQDVRHEEAVASLKNTSDMVY LKVAKPGSLE	341
NeDLG	10863920	3	ILLHKGSTGLGFNIVGGEDGEGIFVSFILAGGPADLSGELR RGDRILSVNGVNLRNATHEQAAAALKRAGQSVTIVAQYR PEEYSRFESKIHDLREQMMNSSMSGSGSLRTSEKRSLE	342
Neurabin II	AJ401189	1	CVERLELFPVELEKDEGLGISIGMGAGADMGLEKLGIFV KTVTEGGAHRDGRIOVNDLLVEVDGTSILVGVTQSFAS VLNRTKGRVRFMIGRERPEQEVAQRIHRD (SEQ ID NO: 343)	343
NOS1	642525	1	IQPNVISVRLFKRKVGGGLFLVKERVSKPPVHISDLIRGGA AEQSGLIQAGDIILAVNGRPLVDLSYDSALEVLGIASETH VVLILRGP	344
novel PDZ gene	7228177	1	QANSDESIIHSVRVEKSPAGRLGFSVRGGSEHGLGIFVSK VEEGSSAERAGLCVGDKITEVNLGLSESTTMGSVAVKVLTS SSRLHMMVRRMGRVPGIKFSKEKNSS	345
novel PDZ gene	7228177	2	PSDTSSDGVRRIVHLYTTSDDFLCFGNIRGGKEFGLGIYV SKVDHGGLAENGIVGQDQVLAANGVRFDIDISHSQAVEV LKGQTHIMLTIKETGRYPAYKEMNSS	346
Novel Serine Protease	1621243	1	KIKKFLTESHDRAKGAATKKKYIGIRMMSLTSSKAKEL KDRHRDPDVISGAYIIEVIPDTPAEAGGLKENDVHISINGQ SVVSANDVSDVIKRESTLNMVRRRGNEDIMITY	347
Numb Binding Protein	AK05682 3	1	PDGEITSIKINRVDPSLSIRLVGGSETPLVHIHQHIYRDG VIARDGRLLPGDHLKVNGMDISNPNHYAVRLLRQPCQV LWLTVMREQKFRSRNSS	348
Numb Binding Protein	AK05682 3	2	HRPRDDSFHVLNKSSPEEQGLIKLVKRVDEPGVFIFNVL GGVAYRHGQLEENDRVLAINGHDLRYGSPESAAILIQAS ERRVHLVVSQRVQRSPENSS	349
Numb Binding Protein	AK05682 3	3	PTTTCHEKVYNIQKDPGESLGMTVAGGASHREWDLPIYVI SVPEGGVISRDGRIKTGDILLNVGDVELTEVSRSEAVALL KRTSSSIVLKALEVKEYEPQEFIV	350
Outer Membrane	7023825	1	LLTEEEINLTRGPSGLGFNIVGGTDQQYVSNDSGIYVSRIK ENGAAALDGRLLQEGDKILSVNGDQLKNLLHQDAVDLFR	351

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
			NAGYAVSLRVQHRLQVQNGIHS	
p55T	12733367	1	PVDAIRILGIHKRAGEPLGVTFRVENNDLVIARILHGGMID RQGLLHVVDIIKEVNGHEVGNNPKELQELIKNISGSVTLK ILPSYRDTITPQQ	352
PAR3	8037914	1	PNFSLDDMVKLVEVPNDGGPLGIHVVPFSARGGRITGLI VVRLEKGGKAHEHENLFRENDICVIRINDGDLRNRFEQAQ HMFQRAMRTPIIWFHVPAANKEQYEQ	353
PAR3	8037914	2	GKRLNIQLKKGTEGLGFSITSRDVTIGGSAPIYVKNILPRG AAIQDGRLLKAGDRLIEVNGVDLVGKSQEEVVSLLRSTKM EGTVSLLVFRQEDA	354
PAR3	8037914	3	PREFLTFEVPLNDSGSAGLGVSVKGNRSKENHADLGIFVK SIINGGAASKDGRRLRVNDQLIAVNGESLLGKTNQDAMET LRRSMSTEGNKRGMQLIVASRISKCNELKSNSS	355
PAR3-like	AF428250	1	PRTKDTLSDMTRTVEISGEGGPLGIHVVPFFSSLSGRII.GI.F IRGIEDNSRSKREGFLFHENECIVKINNVDLVDKTFAQAQD VFERQAMKSPSVLLHVLPPQNR	356
PAR3-like	AF428250	2	SNKNAKKIKIDLKKGPEGLGFTVVTDRSSIHGPGPIFVKNI LPKGAIAKIDGRLQSGDRILEVNGRDTVTRTQEELVAMI.R STKQGETASLVIAREQEH	357
PAR3-like	AF428250	3	ITSEQLTFEIPLNDSGSAGLGVSLLKGNKSRETGTDLGIFIKS IIHGGAAFKDGRRLRMNDQLIAVNGESLLGKSNHEAMETL RRSMSMEGNIRGMQLVILRRPERP	358
PAR6	2613011	1	PETHRRVRLHKHGSDRPLGFYIRDGMSVRVAPQGLERVP GIFISRLVRGGLAESTGLLAVSDEILEVNGIEVAGKTL.DQV TDDMVANSHNLIVTVKPANQRNNVNSS	359
PAR6 BETA	13537116	1	PVSSIIDVDILPETHRRVRLYKYGTEKPLGFYIRDGSSVRV TPHGLEKVPGFISRLVPGGLAQSTGLLAVNDEVLEVNGIIE VSGKSLDQVTDMMIANSRNLITVRPANQRNNRIIRD	360
PAR6 GAMMA	13537118	1	IDVDLVPETHRRVRLHRHGCEKPLGFYIRDGASVRVTPHG LEKVPGFISRMVPGGLAESTGLLAVNDEVLEVNGIEVAG KTL.DQVTDMMIANSHNLIVTVKPANQRNNVV	361
PDZ-73	5031978	1	RSRKLKEVRLDRLHPEGLGLSVRGGLEFGCGLFISHLIKG GQADSVGLQVGDEIVRINGYSISSCTHEEVINLIRTKTVSI KVRHIGLIPVKSSPDEFH	362
PDZ-73	5031978	2	IPGNRENKEKKVFISLVGSRGLGCSISSGPIQKPGIFISHVKP GSLSAEVGLEIGDQIEVNGVDFSNLDHKEAVNVLKSSRS LTSIVAAAGRELFMTEF	363
PDZ-73	5031978	3	PEQIMGKDVRLRLRIKKEGSLDLAEGGVDSPIGKVVVS AV YERGAERHGGVKGDEIMAINGIKIVTDYTLAEADAALQ KAWNQGQGDWIDLVAVCPKKEYDD	364
PDZK1	2944188	1	LTSTFNPRECKLSKQEGQNYGFFLRIEKDTEGHLVRVVEK CSPA EAKAGLQDGRVLRINGVFVDKEEHMQVVDLVRKS GNSVETLLVLDGDSYEKAGSPGIHRD	365
PDZK1	2944188	2	RLCYLVKEGGSYGFSKLTQVGKKGVYMTDITPQGVAMR AGVI.ADDHLIEVNGENVEDASHEEVVEKVKKSGSRVMF LLVDKETDKREFIVTD	366
PDZK1	2944188	3	QFKRETASLKLLPHQPRIVEMKKKGSNGYGFYLRAGSEKQ	367

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PDZK1	2944188	4	GQIIKDIDSGSPAEEAGLKNNDLVVA VNGESVETLDHDSV VEMIRKGGDQTSLLVVDKETDNMYRLAEFIVTD	368
PICK1	4678411	1	PDTTEEVDHDKPKLRLAKGENGYGPHLNAIRGLPGSFIKE VQKGGPADLAGLEDEDVIIENVNGVNVLDPEYKVVDRIQ SSGKNVTLVZGKNSS	369
PIST1	98374330	1	PTVPGKVTLQKDAQNLIIGISIGGGAQYCPCLYIVQVFDNT PAALDGTVAAGDEITGVNGRSIKGKTKVEVAKMIQEVKG EVTIHYNKLQ	370
pril.16	1478492	1	SQGVGPPIRVLLKEDHEGLGISITGGKEHGVPIIISEIHPG QPADRCGGLHVGDAILAVNGVNLDRDTHKKEAVTILSQQR GEIEFEVYVVAPEVDS	371
pril.16	1478492	2	TAEATVCTVTLEKMSAGLGSLEGGKGLSHGDKPLTINRI FKGAASEQSETVQPGDEILQLGGTAMQGLTRFEAWNIIKA LPDGPVTIVIRKSLQSK	372
PSAP	6409315		IREAKYSGVLSSIGKIFKEEGLGGFFVGLIPIHLGDVVFVW GCNLLAHFINAYLVDDSVSDTPGGGLGNDQNGSQFSQAL AIRSYTKFVMGIAVSMPLYPFLVGDIMAVNNCGLQAGL PPYSPVFKSWIHCWKYLSVQGGQLFRGSSLLFRVRSSGSCF ALE	373
PSD95	3318652	1	LEYEeITLERGNSGLGFSIAGGTDNPHIGDDPSIFITKIIPGG AAAQDGRLLRVNDSILFVNEVDVREVTHSAAEVALKEAGS IVRLYVMRRKPPEANSS	374
PSD95	3318652	2	HVMRRKPPAEKVMEIKLIKPGKGLFSIAGGVGNQHPIGD NSIYVTKIIEGGAHKGDRLOIGDKLIANVSVGLEDDVMHE DAVAALKNTYDVVYLKVAKPSNAYLLEFIVTD	375
PSD95	3318652	3	RERHTPRTEANCDDRSGTGLGFNIVGGEDGEGILSPLSWP GALQTSVSGCRGTRSCRSTVWTSEMPAMSRPLP	376
PTN-3	179912	1	QNDNGDSYLVLRITPDEDGKFGFNLKGGVDDQKMPVVS RINPESPADTICPKLNEGDOIVLINGRDISEHTHDQVVMFI KASRESHSRELALVIRRRVRS	377
PTN-4	190747	1	IRMKPDENGFRGFNVKGGYDQKMPVIVSRVAPGTPADLC VPRLENGDQVVLLINGRDIAEHTHDQVVLFIKASCEHSGE LMLLVLPNA	378
PTPL1	515030	1	PEREITLVNLKKDAKYGLGFGIIGGEKMGRLDLGIFISSVA PGGPADFHGCLKPGDRLISVNSVSLGVSHHAAIEILQNA PEDVTLVISQPKKISKVPSTPVHL	379
PTPL1	515030	2	GDIPEVELAKNDNSLGISVTGGVNTSVRHGGIYVKAVIPQ GAAESDGRHKGDRVLAVNGVSLEGATHKQAVETLRNT GQVVHLLLEKQSPSTK	380
PTPL1	515030	3	TEENTFEVKLFKNSSGLGFSFREDNLIPEQINASIVRVKK LFAEQPAAESGKIDVGDVILKVNAGSLKGLSQQEVISALR GTAPVEVFLLCRPPPGVLPEDIT	381
PTPL1	515030	4	EIEVELLITLIKSEKASLGFTVTKGNQRIGCYVHIDVIQDPA KSDGRLLKPGDRLIKVNDTDTVNTMTHTDAVNLLRAASKT VRLVIGRVLELPRIPMLPH	382

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
P1PL1	515030	5	MLPHLLPDITLTCNKEELGFSLCGGHDSLYQVYVYISDINPR SVAIEGNLQLLDVIHYVNGVSTQGMTLEEVNRAIDMSL PSLVLKATRNLDLPV	383
RGS12	3290015	1	RPSPPRVRSVEVARGRAGYGFTLSGQAPCVLSCVMRGSP ADFVGLRAGDQILAVNEINVKKASHEDVVKLIGKCSGV HMVIAEGVGRFESCSNS	384
RGS3	18644735	1	LCSERRYRQITIPRGKDGFGFTICDSPVRVQAVDSGGPAE RAGLQQLDTVLQLNERPVEHWKCVELAEHRSCSPSEIILL VWRMVPQVKPGIHRD	385
Rho-GAP 10	NM02082 4	1	SEDETFSWPGPKTVTLKRTSQGFGFTLRHFIVYPESAIQF SYKDEENGNGRGKQRNRLEPMDTIFVKQVKEGGPAFEA GLCTGDRIIKVNGESVIGKTYSQVIALIQNSDTTLELSVMP KDED	386
Rhopilin- like	14279408	1	SAKNRWRLVGPVHLTRGEGGFLTRGDSPLVIAAVIPGS QAAAAGLKEGDYIVSYNGQPCRWWRAEUVTELKAAG EAGASLQVVSLLPSSRLPSI	387
Serine Protease	2738914	1	RGEKKNSSSGISGSQRRYIGVMMLTLSPSILAELQLREPSF PDVQHGLVLIHKVILGSPAHRAGLRPGDVLAIQEVMQVN AEDVYEAVRTQSQLAVQIRRGRETLLTYVNSS	388
Shank 2	6049185	1	LEETVVLQKKDNEGFGFVLRGAKADTPIEFTPTPAFPA LQYLESVDDEGVAWQAGLRTGDFLIEVNNENNVKVGHR QVVMIRQGGNHLVLKVVTVTRNLDPDDNSS	389
Shank 3	*	1	SDYVIDDKVAVLQKRDEHGFVLRGAKAETPIEFTPTP AFPALQYLESVDVEGVAWRAGLRTGDFLIEVNGVNVVK VGHKQVVALIRQGGNRLVMKVVSVTRKPEEDG	390
Shroom	18652858	1	ISNTATKGRYIYLEAFLEGAPWGFTLKGGLEHGEPLIISK VEEGGKADTLSSKIQAGDEVIIINEVTLSSSRKIEAVSLV KGSYKTLRLVVRDVTCDPGHAD	391
Similar to GRASP65	14286261	1	MGLGVSAEQPAGGAEGFHLHGVQENSPAQQAGLEPYFD FITIGHSRNLNKENDTLKALLKANVEKPVKLEVFNMKTM VREVEVPSNMWGGQGLLGASVRFCFRRASE	392
Similar to GRASP65	14286261	2	RASEQVWHVLDVEPSSPAALAGLRPYTDYVVGSDQILQE SEDFFTLIESHEGKPLKLMVYNSKSDCSRESGMWHVLW VSTDPNSAPQLPQEATWHPTTTCSTWCPTT	393
Similar to Ligand of Numb px2	BC03675 5	1	IQPLSLPEGEITIEIHRSNPYIQLGISIVGGNETPLINIVQEV YRDGVARDGRLLAGDQILQVNNYNSISNVSHSAVLS QPCNTLHLTVLRERRFGNRAH	394
Similar to Ligand of Numb px2	BC03675 5	2	SNSPREEIFQVALHKRDSGEQLGIKLVRRTDPEPGVFILDL EGGLAAQDGRLLSNDRLVLAINGHDLKGTPELAAQIIQAS GERVNLTARPGKPPG	395
Similar to Ligand of Numb px2	BC03675 5	3	QCVTCQEKHITVKKEPHESLGMTVAGGRGSKSGELPIFVT SVPPHGLARLDGRIKRGDVLNNGIDLTNLSHSEAVAMI KASAASPAVALKALEVQIVEAT	396
Similar to Ligand of Numb px2	BC03675 5	4	PSTLHSCHDIVLRRSYLGSWGFISVGGYEENHTNQPFIKT IVLGTPAYYDGRLLKCGDMIVAVNGLSTVGMSHSAIVPM LKEQRNKVTLTVICWPGS	397
Similar to P1P	21595065	1	SVTDGPKFEVKLKKNANGLGFSFVQMEKESCSILKSDLV RIKRLFPQGPAAEENGAIAAGDIILAVNGRSTEGFLIFQEVLIH	398

Gene Name	G1 or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
Homolog			LLRGAPQEVTL LCRPPPGA	
SIP1	2047327	1	QPEPLRPRLCRLVRGEQGYGFHLHGEKGRGQFIRRVEPG SPAEEAALRAGDRLVEVNGVNVEGETHHQVQRIKAVE GQTRLLVVDQETDEELRRNNSS	399
SIP1	2047327	2	PLRELRPRLCHLRKGPQGYGFNLHSDKSRPGQYIRSVDPG SPAARSGRLAQDRLIEVNGQNV EGLRHA EVVASIKAREDE EARLLVVDPETDEHFKNSS	400
SITAC-18	8886071	1	PGVREIHLCKDERGKTGLRLRKVDQGLFVQLVQANTPAS LVGLRFGDQLLQIDGRDCAGWSSHKAHQVVKKASGDKI VVVVDRDPFQRTVTM	401
SITAC-18	8886071	2	PFQRTVTMHKDSMGHVG FVIKKGKIVSLVKGSSAARNGL LTNHYYCEVDGQNVIGLKDKKIMEILATAGNVVTLTIIPS VIYEHIVEFIV	402
SNPC11A	20809633	1	SLERPRFCLLSKEEGKSFGFHLQQLGRAGIIVCRVDPGT SAQRQGLQEGDRLAVNNDVVEHEDYAVVVRIRASSPR VLLTVIARHAHDVARAQ	403
SNPC11A	20809633	3	ISLPTKPRCLHLEKGPQGFGFLREEKGLDGRPGQFLWEV DPGLPAKKAGMQAGDRLVAVAGESVEGLGHEETVSRIQ GGQSCVSLTVVDPEADR	404
SNPC11A	20809633	4	IPSVPLGSRQCFLYPGPGGSYGFRLSCVASGPRLFISQVTP GGSAARAGLQVGDVILEVNGYPVGGQNDLERLQQLPEA EPPLCLKLAARSRLGLE	405
Shank1	7025450	1	LKEKTVLLQKKDSEGFVLRGAKAQTPIEEFTPTAPFA LQYLESVDEGGVAWRAGLRMGDFLIEVNGQNVKVGH RQVYNMIRQGGNTLMVKVVMVTRHPDMDEAVQNSS	406
SYNTENIN	2795862	1	LEIKQGIREVILCKDQDGKIGLR LKSIDNGIFVQLVQANSP ASLVGLRFGDQVLQINGENCAGWSSDKAHKVLKQAFGE KITMRIHRD	407
SYNTENIN	2795862	2	LRDRPFERTITMHKDSGTHGVGFIFKNGKITSIVKDS SAARN GLLTHEHNICEINGQNVIGLKDSQIADILSTSGTVVTITMPAF IFEHMNSS	408
Syntrophin alpha	1145727	1	QRRRVTVRKADAGGLGISIKGGRENKMPILISIKIFKGLAA DQTEALFVGDAILSVNGEDLSSATHDEAVQLKKTGKEV VLEVKYMKDVSPYFK	409
Syntrophin beta 2	476700	1	PVRRVVKQEAAGGLGISIKGGRENRMPIILSIFPGLAADQS RALRLGDAILSVNGTDLRQATHDQAVQALKRAGKEVLL EVKFIRE	410
Syntrophin gamma 1	9507162	1	EPFYSGERTVTIRRTVGGFGLSIKGGAEHNIPVVVSKISK EQRAELSGLLFIGDAILQINGINVRKCRHEEVVQVLNRAG EEVTLTVSFLKRAPAFILKP	411
Syntrophin gamma 2	9507164	1	SHQGRNRRTVTLRQPVGGLGLSIKGGSEHNVPVVISKIF EDQAADQTGMLFVGDAVLQVNGIHVENATHEEVVHLLR NAGDEVTTTVEYLREAPAFK	412
TAX2-like protein	3253116	1	RGETKEVEVTKTEDALGLTITDNGAGYAFIKRIKEGSIINRI EAVCVGDSIEAINDHSIVGCRHYEVAKMLRELPSQPFIL RLVQPKRAF	413
TIAM 1	4507500	1	HSIHIEKSDTAADTYGFSLSVVEEDGIRRLVNSVKETGLA	414

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO.
			SKKGLKAGDEILEINNRAADALNSSMLKDFLSQPSLGI.LV RTYPELE	
TIAM 2	6912703	1	PLNVYDVQLTKTGSVCDGFAVTAQVDERQHLSRIFISDV LPDGI.AYGEGLRKGNEMITLNGEAVSDDLKQMEALFSE KSVGLTLIARPPDTKATL	415
TIP1	2613001	1	QRVEIHKLRQGENLILGFSIGGGIDQDPSONPFSEDKTDKG IYVTRVSEGGPAEIAGLQIGDKIMQVNGWDMTMTVTIDQ ARKRLTKRSEEVVRLVTRQSLQK	416
TIP2	2613003	1	RKEVEVFKSEDALGLTITDNGAGYAFIKRIKEGSVIDHIIIL ISVGMIEAINGQSLLGCRHIYEVARLLKELPRGRITTLKI. TEPRK	417
TIP33	2613007	1	IISHPRVVELPKTDEGLGFNMGGKEQNSPIYISRIIPGGVA ERHGGGLKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDS VKLVVRYTPKVL	418
TIP43	2613011	1	LSNQKRGVKVLKQELGGLGISIKGGKENKMPILISKIFKGL AADQTQALYVGDAILSVNGADLRDATHDEAVQALKRAG KEVLLLEVKKYMRATPYVKNSS	419
Unknown PDZ gene		1	QRSSIKTVELIKGNLQSVGLTLRLVQSTDGYAGHVIIETVA PNSPAADIADLRQGDRLIAIGGVKITSTLQVLKLIKQAGDRV LVYYERPVGQSNQGA	420
X-11 beta	3005559	1	IHFNSNENCKELQLEKHKGEILGVVVVESGWSILPTVILA NMMNGGPAARSGKLSIGDQIMSINGTSLVGLPLATCQGII KGLKNQQTQVKLNIVSCPPVTTLIKRNS	421
X-11 beta	3005559	2	IPPVTTVLIKRPDLKYQLGFSVQNGHICSLMRGGIAERGGV RVGHRHIEINGQSVVATAHEKIVQALNSNSVGEIIMKTPMA AMFRLLTGQENSS	422
ZO-1	292937	1	IWEQHTVTLHRAPGFGFGIAISGGGRDNPHFQSGETSIVISD VLKGGPAEGQLQENDRVAMVNGVSMDNVEHAFVQQL RKSGKNAKITIRKKKKVQIPNSS	423
ZO-1	292937	2	ISSQPAKPTKVTLVKSRLNVEYGLRLASHIFVKEISQDSL ARDGNIQEGDVVLKINGTVTENMSLTDAKTLIERSKGKL KMVVQRDRATLLNSS	424
ZO-1	292937	3	IRMKLVKFRKGDSVGLRLAGGNDVGIFVAGVLEDSPA EGLEEGDQILRVNNVDFTNIIREEAVLFLDLPKGEEVTIL AQKKKDVFSN	425
ZO-2	12734763	1	LIWEQYTVTLQKDSKRGFGIAVSGGRDNPHFENGETSIVIS DVLPGGPADGLLQENDRVVMVNGTPMEDVLHSAFVQQL RKSGKVAIVVKRPKV	426
ZO-2	12734763	2	RVLLMKSRANEYGLRLGSQIFVKEMTRTGLATKDGNLH EGDILKINGTVTENMSLTDARKLIEKSRGKLQVLVLRDS	427
ZO-2	12734763	3	IAPNTKMVRFFKKGDSVGLRLAGGNDVGIFVAGIQEGTSA EQEGLQEGDQILKVTQDFRGLVREDAVLYLLEIPKGEIM VTILAQSRADVY	428
ZO-3	10092690	1	IPGNSTIWEQHTATLSKDPRRGFGIAISGGDRDPGGSMVV SDVVPGGPAEGRLOTGDHIVMVNGVSMENATSAFAIQIL KTCTKMANITVKRPRIHLPAAEFIVTD	429
ZO-3	10092690	2	QDVQMKPVKSVLVKRRDSEEFVKLGSGQIFIKHITDSGLA ARHRLQEGDLILQINGVSSQNLSLNDTRRLIEKSEGLSL	430



Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
			LVLDRGQFLVNIPNSS	
ZO-3	100926903	3	RGYSPDTRVVRFLKGKISIGLRLAGGNDVGIFVSGVQAGSP ADGGGIGQEGDQILQVNDVPFQNLTREEAVQFLGLPPGEE MELVTQRKQDIFWKMVQSEFIVTD	431

\*: No GI number for this PDZ domain containing protein - it was computer cloned by J.S. using rat Shank3 seq against human genomic clone AC000036. In silico spliced together nt6400-6496, 6985-7109, 7211-7400 to create hypothetical human Shank3.

At page 49 through page 50, please replace Table 4 with the following Table 4:

**TABLE 4**

Primers used in cloning of RIM2 PDZ domain 1.

ID# (Primer Name)	Primer Sequence	Description	Seq ID
1968 (688KIFlo)	AAAGATCTCCCTTA ACGAGGAGCATAG	Forward (5' to 3') primer corresponding to RIM2, domain 1. Generates a BglII site upstream (5') of the PDZ boundary. Used for cloning into pGEX-3X.	273 432
1093 (319 KIR)	GAACAATTGCAATA GGCCTTGAACTAC	Reverse (3' to 5') primer corresponding to RIM2, domain 1. Generates a MfeI site downstream (3') of the PDZ boundary. Used for cloning into pGEX-3X.	274 434

At page 50, lines 2 through lines 9, please replace the paragraph with the following paragraph:

**RIM2, PDZ domain 1:** GI#: 12734165; Construct: RIM2, PDZ domain 1-pGEX-3X; primers: 1968 & 1093; Vector Cloning Sites (5'/3'): Bam HI/EcoRI; Insert Cloning Sites(5'/3'): BglII/MfeI  
aa 1 - aa 126

TLNNEEHSIISDKHPVTWQPSKDGDRLLGRILLNKRLKDGSVPRDSGAMLGLKVVGGMKT  
ESGRICAFITKVKKGLADTVGHILRPGDEVLEWNGRLLQGATFEVYNIILESKPEPQVIE  
L.VVSRPIG (SEQ ID NO:437)

At page 54 through page 59, please replace Table 5 with the following Table 5

**Table 5**  
Oligonucleotide primers used for RT-PCR

AVC No	Oligo Name	Sequence	SEQ ID NO.	Description
3303	Zo-3 dom3 FA	Gcatccaggaggagatcag	437	forward amplicon primer
3302	Zo-3 dom3 RA	aggttctggaatggcacgtc	438	reverse amplicon primer
3301	Zo-3 dom3 FB	ggcgcacagaggaggagat	439	forward amplicon primer
3300	Zo-3 dom3 RB	caggttctggaatggcacg	440	reverse amplicon primer
3299	Zo-3 dom1 FA	caggcgaccacatcgctat	441	forward amplicon primer
3298	Zo-3 dom1 RA	gaggtggcattctccatgga	442	reverse amplicon primer
3297	Zo-3 dom1 FB	tccatggagaatgccacctc	443	forward amplicon primer
3296	Zo-3 dom1 RB	ccatcttggtgcaggcttga	444	reverse amplicon primer
3295	Zo-2 dom1 FA	agtggtcatggtcaatggca	445	forward amplicon primer
3294	Zo-2 dom1 RA	gcaaacgaatgaagcacatcc	446	reverse amplicon primer
3293	Zo-2 dom1 FB	ctgatggctctgcctcaaga	447	forward amplicon primer
3292	Zo-2 dom1 RB	gggtgcccattgacctgac	448	reverse amplicon primer
3291	Zo-2 dom2 FA	agtatggctccggcttgagg	449	forward amplicon primer
3290	Zo-2 dom2 RA	tccgggtcattctcttacga	450	reverse amplicon primer
3289	Zo-2 dom2 FB	gatgaaaagcagagcgaaacga	451	forward amplicon primer
3288	Zo-2 dom2 RB	cgaagatctgactcccaagcc	452	reverse amplicon primer
3252	KIA0340 DOM 1 2ND R	caaccaagtcctctaagtcagcat	453	reverse amplicon primer
3251	KIA0340 DOM 1 2ND F	ctgggtctgaaagttgtggagg	454	forward amplicon primer
3250	GRIP2 DOM 5 2ND R	cagttgtccaggcggatattg	455	reverse amplicon primer
3249	GRIP2 DOM 5 2ND F	ggagccaggcgcacaagc	456	forward amplicon primer
3248	LIM MYST DOM 1 2ND R	cggtgatggccagcattatgt	457	reverse amplicon primer
3247	LIM MYST DOM 1 2ND F	aaagccaaaggacgctgacct	458	forward amplicon primer
3246	KIA0316 DOM 1 2ND R	aggagtatcgtattcttgacgtt	459	reverse amplicon primer
3245	KIA0316 DOM 1 2ND F	ccagagagcgggtcatcgatc	460	forward amplicon primer
3244	MAGI2 DOM5 2ND R	tcctaccctcatctcccat	461	reverse amplicon primer
3243	MAGI2 DOM5 2ND F	agactggcagaagatggacca	462	forward amplicon primer
3242	MAST1 DOM 1 2ND R	tccgtgtcaccatgtagacac	463	reverse amplicon primer
3241	MAST1 DOM 1 2ND F	gaagtatgcttcaactcgct	464	forward amplicon primer
3240	MINT3 COMPL 2ND R	catgcctgactccaggct	465	reverse amplicon primer
3239	MINT3 COMPL 2ND F	cgatttgggaactgcctgaa	466	forward amplicon primer
3238	MUPP1 DOM 3 2ND R	caatgtagccagcaatggaattc	467	reverse amplicon primer
3237	MUPP1 DOM 3 2ND F	gaactcactaaaatgtccaaggattag	468	forward amplicon primer
3236	NOVEL PDZ DOM 1	ccatggtggtgctctccag	469	reverse amplicon primer

AVC			SEQ ID	
No	Oligo Name	Sequence	NO	Description
	2ND R			
	NOVEL PIDZ DOM I		<u>470</u>	
3235	2ND F	gggacaagatcacggaggtg		forward amplicon primer
3234	NSP DOM 1 2ND R	cgtcctctgagatcacgtctg	<u>471</u>	reverse amplicon primer
3233	NSP DOM 1 2ND F	aaagagctgaaggaccggc	<u>472</u>	forward amplicon primer
3232	HER1 2ND R	tgccatcacgtaggcttc	<u>473</u>	reverse amplicon primer
3231	HER1 2ND F	agcaacatctccgaagcca	<u>474</u>	forward amplicon primer
	SYNTROPHINY DOM		<u>475</u>	
3230	I R	tcagctgcttggcttcgaat		reverse amplicon primer
	SYNTROPHINY DOM		<u>476</u>	
3229	I F	gcacaacgtccctgtctgtc		forward amplicon primer
3228	PRIL16 DOM I R	cgttgctcccttgagagactt	<u>477</u>	reverse amplicon primer
3227	PRIL16 DOM I F	aaggccaatgaggtctcttc	<u>478</u>	forward amplicon primer
3226	KIA 1719 DOM 5 R	gcagttgtccaggcggata	<u>479</u>	reverse amplicon primer
3225	KIA 1719 DOM 5 F	gagccaggcgacaagctact	<u>480</u>	forward amplicon primer
3224	KIA1526 DOM I R	cccgagctcttctcttc	<u>481</u>	reverse amplicon primer
3223	KIA1526 DOM I F	acgtgtctctgttggaaaccag	<u>482</u>	forward amplicon primer
3222	FGFR3 IIIC B NEW R	gcacgtccagcgtgtacgt	<u>483</u>	reverse amplicon primer
3221	FGFR3 IIIC B NEW F	tgtctgtgtgagagaacgttt	<u>484</u>	forward amplicon primer
3220	FGFR3 IIIC A NEW R	acgtccagcgtgtacgtctg	<u>485</u>	reverse amplicon primer
3219	FGFR3 IIIC A NEW F	cgctgtggagacaagttgg	<u>486</u>	forward amplicon primer
3218	HER2 B NEW R	ccacttgatggcagcttgc	<u>487</u>	reverse amplicon primer
3217	HER2 B NEW F	ctgtgtgacattgacgagaca	<u>488</u>	forward amplicon primer
3216	HER2 A NEW R	ctgtgtacgagccgacatc	<u>489</u>	reverse amplicon primer
3215	HER2 A NEW F	ctgtgtgatgcagattgccaa	<u>490</u>	forward amplicon primer
	VARTUL COMPLETE		<u>491</u>	
3214	R	cagatcgttgctcccagat		reverse amplicon primer
	VARTUL COMPLETE		<u>492</u>	
3213	F	cgctcctgtcattctgtgtca		forward amplicon primer
3212	SITAC18 DOM I R	tgccttcttcaccacctgatg	<u>493</u>	reverse amplicon primer
3211	SITAC18 DOM I F	gactgtgtctgggtggagctc	<u>494</u>	forward amplicon primer
3210	DLG 1 DOM 2 R	ccgagacaatgtctgattcca	<u>495</u>	reverse amplicon primer
3209	DLG 1 DOM 2 F	ggctcttgggttagcattgctg	<u>496</u>	forward amplicon primer
3208	DLG 1 DOM 1 R	tctccaatgtgtgtgtgtgcc	<u>497</u>	reverse amplicon primer
3207	DLG 1 DOM 1 F	tcaggcgttggttcagcat	<u>498</u>	forward amplicon primer
3206	Ubiquitin R Chamorro	caattgggaatgcacaactttat	<u>499</u>	reverse amplicon primer
3205	Ubiquitin F Chamorro	cacttggtcctgcgctga	<u>500</u>	forward amplicon primer
3204	Ubiquitin F	aatcatttgggtcaatatgtaatttca	<u>501</u>	forward amplicon primer
3203	Ubiquitin R	gcggacaatttactgtactaacactga	<u>502</u>	reverse amplicon primer
3202	18S RNA R	gggtcgggagtggtgaattt	<u>503</u>	reverse amplicon primer
3201	18S RNA F	ctaccacatccaagggaagca	<u>504</u>	forward amplicon primer
3200	P1PL1 dom4 R	cttttgctggtatcctgtatgac	<u>505</u>	reverse amplicon primer
3199	P1PL1 dom4 F	tcagagaattgggtgttatgttcag	<u>506</u>	reverse amplicon primer
3198	Mupp1 dom 6 R	tcggccatctgcactaatg	<u>507</u>	reverse amplicon primer
3197	Mupp1 dom 6 F	gggatgatcgttccaagcat	<u>508</u>	forward amplicon primer
3196	Mast 3 com 1 R	agacgtgcctatcaccaatgt	<u>509</u>	reverse amplicon primer
3195	Mast 3 dom 1 F	tggaagaagtacgggttca	<u>510</u>	forward amplicon primer
3194	Kia340 dom 1 R	aacaactttcagaccagcaatg	<u>511</u>	reverse amplicon primer
3193	Kia340 dom 1 F	agaacaacatgcccaagact	<u>512</u>	forward amplicon primer

AVC			SEQ ID	
No	Oligo Name	Sequence	NO'	Description
3192	INAD1. dom 3 R	ctgcctcgtcatttcgtaa	<a href="#">513</a>	reverse amplicon primer
3191	INAD1. dom 3 F	cagggttttgccaacatg	<a href="#">514</a>	forward amplicon primer
3190	PAR 3 dom 3 R	gcccaacagggtattcctat	<a href="#">515</a>	reverse amplicon primer
3189	PAR3 dom 3 F	ggcttcgggtgaatgatcaa	<a href="#">516</a>	forward amplicon primer
3188	Pick 1 dom 1 R	cttcgccactccaccattag	<a href="#">517</a>	reverse amplicon primer
3187	Pick 1 dom 1 F	ggtgtcaatggcaggtcaatc	<a href="#">518</a>	forward amplicon primer
3186	RGS3 dom 1 R	gaatccacggcgtggaactc	<a href="#">519</a>	reverse amplicon primer
3185	RGS3 dom 1 F	tggcttcaccatctcgtgc	<a href="#">520</a>	forward amplicon primer
3184	Sip 1 dom 1 R	cagccttgatcctttgcacc	<a href="#">521</a>	reverse amplicon primer
3183	Sip 1 dom 1 F	gtcaacgtggaggcgag	<a href="#">522</a>	forward amplicon primer
3182	SIP1 dom 2 R	gccgggactgtcactatgc	<a href="#">523</a>	reverse amplicon primer
3181	SIP 1 dom 2 F	gaaggaggacctgaggctatg	<a href="#">524</a>	forward amplicon primer
3180	Tip 1 R	ccaatgctgaaccaggat	<a href="#">525</a>	reverse amplicon primer
3179	Tip 1 F	aattccaagaactgcgtcaagg	<a href="#">526</a>	forward amplicon primer
3178	AIPC dom 1 F	gggccttgctttagtatgc	<a href="#">527</a>	forward amplicon primer
3177	Mint 3 500 bp R	cagctggcatcgtcttgatag	<a href="#">528</a>	reverse amplicon primer
3176	Mint 3 500bp F	agctgtcaccgaggcctat	<a href="#">529</a>	forward amplicon primer
3175	Mint 1 dom2 R	cgcatagggctgcagataatt	<a href="#">530</a>	reverse amplicon primer
3174	Mint 1 dom2 F	ctaccagctcggtttcacgg	<a href="#">531</a>	forward amplicon primer
3173	Mint 1 dom1 R	tctggcaggtggacagagg	<a href="#">532</a>	reverse amplicon primer
3172	Mint 1 dom1 F	cggtagcacaatcatctccat	<a href="#">533</a>	forward amplicon primer
3171	P1N3 R	acgatttagtcccctctgttc	<a href="#">534</a>	reverse amplicon primer
3170	P1N3 F	agtcacctgcggacacctg	<a href="#">535</a>	forward amplicon primer
3169	HTRA2 R	gggaaagcttggttctgaag	<a href="#">536</a>	reverse amplicon primer
3168	HTRA2 F	ctgagtcaccagcatccttc	<a href="#">537</a>	forward amplicon primer
3167	AIPC dom 1 R	ccccatctgtccagaatg	<a href="#">538</a>	reverse amplicon primer
3166	Mast 2 dom 1 F	acttcttgcagcccttgg	<a href="#">539</a>	forward amplicon primer
3165	Mupp1 dom 3 R	tgtgtctccaatttgattcttc	<a href="#">540</a>	reverse amplicon primer
3164	Mupp1 dom 3 F	acaaaaagcagtgccgttga	<a href="#">541</a>	forward amplicon primer
3163	Novel PDZ dom 1 R	cagcaccittacggcgctac	<a href="#">542</a>	reverse amplicon primer
3162	Novel PDZ dom 1 F	aatggccttgagcctggaga	<a href="#">543</a>	forward amplicon primer
3161	MAG1 2 dom 5 F	tgtggacatggagaaaggagc	<a href="#">544</a>	forward amplicon primer
3160	Mast 1 dom 1 R	tgcagacaatgttggtggac	<a href="#">545</a>	reverse amplicon primer
3159	Mast 1 dom 1 F	tgtctacattgggtgacacgga	<a href="#">546</a>	forward amplicon primer
3158	Mast 2 dom 1 R	gctcgggtggatgatgatgg	<a href="#">547</a>	reverse amplicon primer
3157	NSP dom 1 R	tcttgagatcacgtctgggaa	<a href="#">548</a>	reverse amplicon primer
3156	NSP dom 1 F	aagccaaagagctgaagagacc	<a href="#">549</a>	forward amplicon primer
3155	Elfin 1 dom 1 R	ccctgtctccaggagtgacc	<a href="#">550</a>	reverse amplicon primer
3154	Elfin 1 dom 1 F	aaaggactctgagcagcctct	<a href="#">551</a>	forward amplicon primer
3153	EBP50 dom 2 R	tccactgaccggatgaactg	<a href="#">552</a>	reverse amplicon primer
3152	EBP50 dom 2 F	caacctgcacagcgacaagt	<a href="#">553</a>	forward amplicon primer
3151	ZO 1 dom 2 R	gcttgcacatcgaaacacat	<a href="#">554</a>	reverse amplicon primer
3150	ZO 1 dom 2 F	acactgggtgaatcccgga	<a href="#">555</a>	forward amplicon primer
3149	EBP50 dom 1 R	tgtactggcccaacttgc	<a href="#">556</a>	reverse amplicon primer
3148	EBP50 dom 1 F	agaaggggtccgaagcgctac	<a href="#">557</a>	forward amplicon primer
3147	APX1. dom 1 R	cgcttctgtctaaacctga	<a href="#">558</a>	reverse amplicon primer
3146	APX1. dom 1 F	tgagatcgtcgcatcaatg	<a href="#">559</a>	forward amplicon primer

AVC No	Oligo Name	Sequence	SEQ ID NO'	Description
3145	Grip 2 dom 5 R	gcagttgtccaggcggata	<u>560</u>	reverse amplicon primer
3144	Grip 2 dom 5 F	gagccagcgcacaagctact	<u>561</u>	forward amplicon primer
3143	KIA0382 dom 1 R	atggctgtctcatctcttttg	<u>562</u>	reverse amplicon primer
3142	KIA0382 dom 1 F	cggtcagttggagacaatcca	<u>563</u>	forward amplicon primer
3141	l:bin dom 1 R	acaccactgtatgtctaatcca	<u>564</u>	reverse amplicon primer
3140	l:bin dom 1 F	agtgaagggttgaagaaggatcca	<u>565</u>	forward amplicon primer
3139	KIA0316 dom 1 R	tgaccagatcgatgacccg	<u>566</u>	reverse amplicon primer
3138	KIA0316 dom 1 F	aatgatgaaccgggtcagcg	<u>567</u>	forward amplicon primer
3137	KIA0751(RIM2) dom 1 R	aaagccgacctgattcagtc	<u>568</u>	reverse amplicon primer
3136	F	caatgcttggcttgaagggttg	<u>569</u>	forward amplicon primer
3135	Lim Mystique dom 1R	ccgttgatggccacgattat	<u>570</u>	reverse amplicon primer
3134	Lim Mystique dom 1F	agcccaaggacgctgacctc	<u>571</u>	forward amplicon primer
3133	Lim Protein dom 1 R	ccttccgccatctttttaga	<u>572</u>	reverse amplicon primer
3132	Lim Protein dom 1 F	cggtgaagatttcaacatgcc	<u>573</u>	forward amplicon primer
3131	MAG1 2 dom 5 R	cctcccaagatctggaatcc	<u>574</u>	reverse amplicon primer
3116	AIPC As (reverse)	gtgatccatttgggaagatg	<u>575</u>	Amplicon primer for real-time PCR
3115	AIPC S (forward)	gcattcgtgacagatggg	<u>576</u>	Amplicon primer for real-time PCR
3114	HER 1 As (reverse)	cagggatccgcatatggct	<u>577</u>	Amplicon primer for real-time PCR
3113	HER 1 S (forward)	ccgtttgggagttgatgacc	<u>578</u>	Amplicon primer for real-time PCR
3112	HER 2 As (reverse)	ccatttgaaggcaccttg	<u>579</u>	Amplicon primer for real-time PCR
3111	HER 2 S (forward)	tgtctgacattgacgagacag	<u>580</u>	Amplicon primer for real-time PCR
3110	FGFR3C AS (reverse)	cacgtccagcgtgtacgtct	<u>581</u>	Amplicon primer for real-time PCR
3109	FGFR3C S (forward)	ctgcgtctgtggaacaacgtt	<u>582</u>	Amplicon primer for real-time PCR
3108	b-Catenin AS (reverse)	gctgggtatcctgatgtgca	<u>583</u>	Amplicon primer for real-time PCR
3107	b-Catenin S (Forward)	gggtgccattccacgactag	<u>584</u>	Amplicon primer for real-time PCR
3106	MUC-1 AS (reverse)	tgtccagctgccctgatttc	<u>585</u>	Amplicon primer for real-time PCR
3105	MUC-1 S (forward)	tgccttggctgtctgtcag	<u>586</u>	Amplicon primer for real-time PCR
3414	RIM2 P7R	tgtggttcaggttggattctaga	<u>587</u>	
3413	RIM2 P7F	cacatttgaggaaaggtacacatcat	<u>588</u>	
3412	RIM2 P6R	tggctctctgtagtagcttcc	<u>589</u>	
3411	RIM2 P6F	gaccaggtgtagaagtattagaatgg	<u>590</u>	
3410	RIM2 P5R	ccaccaagtagcatatttctttt	<u>591</u>	
3409	RIM2 P5F	gtcggactctaacaccagggtctg	<u>592</u>	
3408	RIM2 P4R	tggccaccacaagtagcatatttc	<u>593</u>	
3407	RIM2 P4F	ctctaaccaggctctgagagacaaa	<u>594</u>	
3406	RIM2 P3R	ttagttccatttgggttcca	<u>595</u>	
3405	RIM2 P3F	tccagacagaagtgataaacaagag	<u>596</u>	
3404	RIM2 P2R	tgcattgttaggtttgttcca	<u>597</u>	
3403	RIM2 P2F	ccaccaaatatctacaaaatgagctt	<u>598</u>	
3402	RIM2 P1R	tccagatcagcattgtccaa	<u>599</u>	
3393	RIM2 P1F	acggcatgagagaaggcatag	<u>600</u>	